



## SEQUENCE LISTING

<110> Stein, Bernd  
Yang, Maria X. H.

<120> MITOGEN-ACTIVATED PROTEIN KINASE KINASE  
MEK6 AND METHODS OF USE THEREFOR

<130> 860098.403C1

<140> US 09/593,288

<141> 2000-06-13

<150> US 08/576,240

<151> 1995-12-20

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1002  
<212> DNA  
<213> homo sapien

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<221> CDS  
<222> (1)...(1002)

<400> 1  
atg tct cag tcg aaa ggc aag aag cga aac cct ggc ctt aaa att cca 48  
Met Ser Gln Ser Lys Gly Lys Lys Arg Asn Pro Gly Leu Lys Ile Pro  
1 5 10 15  
aaa gaa gca ttt gaa caa cct cag acc agt tcc aca cca cct cga gat 96  
Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp  
20 25 30  
tta gac tcc aag gct tgc att tct att gga aat cag aac ttt gag gtg 144  
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val  
35 40 45  
aag gca gat gac ctg gag cct ata atg gaa ctg gga cga ggt gcg tac 192  
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr  
50 55 60  
ggg gtg gtg gag aag atg cgg cac gtg ccc agc ggg cag atc atg gca 240  
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala  
65 70 75 80  
gtg aag cgg atc cga gcc aca gta aat agc cag gaa cag aaa cgg cta 288  
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu  
85 90 95  
ctg atg gat ttg gat att tcc atg agg acg gtg gac tgt cca ttc act 336

Leu Met Asp	Leu Asp Ile Ser Met	Arg Thr Val Asp Cys Pro Phe Thr	
100	105	110	
gtc acc ttt tat ggc gca ctg ttt cgg gag ggt gat gtg tgg atc tgc			384
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys			
115	120	125	
atg gag ctc atg gat aca tca cta gat aaa ttc tac aaa caa gtt att			432
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile			
130	135	140	
gat aaa ggc cag aca att cca gag gac atc tta ggg aaa ata gca gtt			480
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val			
145	150	155	160
tct att gta aaa gca tta gaa cat tta cat agt aag ctg tct gtc att			528
Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile			
165	170	175	
cac aga gac gtc aag cct tct aat gta ctc atc aat gct ctc ggt caa			576
His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln			
180	185	190	
gtg aag atg tgc gat ttt gga atc agt ggc tac ttg gtg gac tct gtt			624
Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val			
195	200	205	
gct aaa aca att gat gca ggt tgc aaa cca tac atg gcc cct gaa aga			672
Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg			
210	215	220	
ata aac cca gag ctc aac cag aag gga tac agt gtg aag tct gac att			720
Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile			
225	230	235	240
tgg agt ctg ggc atc acg atg att gag ttg gcc atc ctt cga ttt ccc			768
Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro			
245	250	255	
tat gat tca tgg gga act cca ttt cag cag ctc aaa cag gtg gta gag			816
Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu			
260	265	270	
gag cca tog cca caa ctc cca gca gac aag ttc tct gca gag ttt gtt			864
Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val			
275	280	285	
gac ttt acc tca cag tgc tta aag aag aat tcc aaa gaa cgg cct aca			912
Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr			
290	295	300	
tac cca gag cta atg caa cat cca ttt ttc acc cta cat gaa tcc aaa			960
Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys			
305	310	315	320
gga aca gat gtg gca tct ttt gta aaa ctg att ctt gga gac			1002
Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp			

325

330

<210> 2  
 <211> 333  
 <212> PRT  
 <213> homo sapien

<400> 2  
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 Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp Leu  
 20 25 30  
 Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val Lys  
 35 40 45  
 Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr Gly  
 50 55 60  
 Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala Val  
 65 70 75 80  
 Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu Leu  
 85 90 95  
 Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr Val  
 100 105 110  
 Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys Met  
 115 120 125  
 Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile Asp  
 130 135 140  
 Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val Ser  
 145 150 155 160  
 Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile His  
 165 170 175  
 Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln Val  
 180 185 190  
 Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val Ala  
 195 200 205  
 Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg Ile  
 210 215 220  
 Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile Trp  
 225 230 235 240  
 Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro Tyr  
 245 250 255  
 Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu Glu  
 260 265 270  
 Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val Asp  
 275 280 285  
 Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr Tyr  
 290 295 300  
 Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys Gly  
 305 310 315 320  
 Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp  
 325 330

<210> 3  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> 5' specific forward primer

<400> 3  
ttgtgctccc ctcccccatc aaaggaa

27

<210> 4  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Reverse 5' PCR primer

<400> 4  
cacatcttca cttgaccgag agca

24

<210> 5  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' primers of human p38

<400> 5  
ccaacccatgg ctcaggagag

20

<210> 6  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' Primer of human p38

<400> 6  
cggtaccttc aggactccat ct

22